

Amendment to the Claims

This listing of claims will replace all prior versions and listings of claims.

What Is Claimed Is:

1. (Currently amended) Use of a polypeptide for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a medical condition, wherein said polypeptide comprises an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:
 - (a) amino acid residues 1 to 150 a full length polypeptide of SEQ ID NO:282 SEQ ID NO:Y or a full length polypeptide encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845 ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A;
 - (b) amino acid residues 24 to 150 a predicted secreted form of SEQ ID NO:282 SEQ ID NO:Y or a secreted form of the polypeptide encoded by the cDNA Clone ID in ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A;
 - (c) a mature polypeptide a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845 ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A;
 - (d) a polypeptide fragment of SEQ ID NO:282 SEQ ID NO:Y, wherein said fragment is at least 30 contiguous amino acid residues or a polypeptide fragment encoded by the cDNA Clone ID in ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A, wherein said fragment has biological activity;
 - (e) a polypeptide fragment of SEQ ID NO:282, wherein said fragment is at least 50 contiguous amino acid residues a polypeptide domain of SEQ ID NO:Y as referenced in Table 1B;
 - (f) a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845, wherein said fragment is at least 30 contiguous amino acid residues a polypeptide domain of SEQ ID NO:Y as referenced in Table 2; and
 - (g) a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845, wherein said fragment is at least 50 contiguous amino acid residues a predicted epitope of SEQ ID NO:Y as referenced in Table 1B.
2. (Original) Use of the polypeptide of claim 1, wherein said polypeptide comprises a heterologous amino acid sequence.

3-6 (Canceled).

7. (Currently Amended) A polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

- (a) amino acid residues 1 to 150a full length polypeptide of SEQ ID NO:282SEQ ID NO:Y or a full length polypeptide encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A;
- (b) amino acid residues 24 to 150a predicted secreted form of SEQ ID NO:282SEQ ID NO:Y or a secreted form of the polypeptide encoded by the cDNA Clone ID in ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A;
- (c) a mature polypeptidea polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A;
- (d) a polypeptide fragment of SEQ ID NO:282SEQ ID NO:Y, wherein said fragment is at least 30 contiguous amino acid residues or a polypeptide fragment encoded by the cDNA Clone ID in ATCC Deposit No:Z corresponding to SEQ ID NO:Y as referenced in Table 1A, wherein said fragment has biological activity;
- (e) a polypeptide fragment of SEQ ID NO:282, wherein said fragment is at least 50 contiguous amino acid residuesa polypeptide domain of SEQ ID NO:Y as referenced in Table 1B;
- (f) a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845, wherein said fragment is at least 30 contiguous amino acid residuesa polypeptide domain of SEQ ID NO:Y as referenced in Table 2; and
- (g) a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845, wherein said fragment is at least 50 contiguous amino acid residuesa predicted epitope of SEQ ID NO:Y as referenced in Table 1B.

8. (Original) The polypeptide of claim 7, wherein said polypeptide comprises a heterologous amino acid sequence.

9. (Original) Use of the polypeptide of claim 7 for identifying a binding partner comprising:

- (a) contacting the polypeptide of claim 7 with a binding partner; and
- (b) determining whether the binding partner increases or decreases activity of the polypeptide.

10-14. (Canceled)

15. (New) A polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) amino acid residues 1 to 150 of SEQ ID NO:282 or a full length polypeptide encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845;
- (b) amino acid residues 24 to 150 of SEQ ID NO:282;
- (c) a mature polypeptide encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845;
- (d) a polypeptide fragment of SEQ ID NO:282, wherein said fragment is at least 30 contiguous amino acid residues;
- (e) a polypeptide fragment of SEQ ID NO:282, wherein said fragment is at least 50 contiguous amino acid residues;
- (f) a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845, wherein said fragment is at least 30 contiguous amino acid residues; and
- (g) a polypeptide fragment encoded by the HCPCB26 cDNA Clone ID in ATCC Deposit No:PTA-3845, wherein said fragment is at least 50 contiguous amino acid residues.

16. (New) The polypeptide of claim 15, wherein said polypeptide comprises a heterologous amino acid sequence.

17. (New) The polypeptide of claim 7, wherein said polypeptide is glycosylated.

18. (New) The polypeptide of claim 15, wherein said polypeptide is glycosylated.

19. (New) An isolated polypeptide produced by the method comprising:

- (a) expressing the polypeptide of claim 7 by a cell; and

(b) recovering said polypeptide.

20. (New) An isolated polypeptide produced by the method comprising:
 - (a) expressing the polypeptide of claim 15 by a cell; and
 - (b) recovering said polypeptide.
21. (New) Use of the polypeptide of claim 15 for identifying a binding partner comprising:
 - (a) contacting the polypeptide of claim 15 with a binding partner; and
 - (b) determining whether the binding partner increases or decreases activity of the polypeptide.